

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 27, 2001, 16:42:23 ; Search time 26.6 Seconds

(without alignments)  
933.568 Million cell updates/sec

Title: US-09-483-543a-9

Perfect score: 1733

Sequence: 1 KRGCAGNEDSERSSWYGR.....SGCGXGLEVLFGQPVKRGXG 326

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_68:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1612	93.0	304	2 I58394	C-Crk - mouse
2	1588	91.6	304	2 A45022	CRK-II - human
3	1379.5	79.6	305	1 A49011	c-Crk - chicken
4	1078	62.2	239	2 A46243	epidermal growth f
5	1052	60.7	204	2 B45022	CRK-1 - human
6	917.5	52.9	303	2 S41754	CRKL protein - hum
7	911.5	52.6	303	2 S58352	SH2/SH3 adaptor pr
8	834.5	48.2	259	2 A44988	transforming prote
9	818.5	47.2	232	1 TVFV10	transforming prote
10	236	13.6	211	2 A46444	SH2-SH3 adaptor pr
11	224	12.9	217	2 S26050	growth factor rece
12	224	12.9	217	2 A54688	modular adaptor Gr
13	224	12.9	217	2 A43321	growth factor rece
14	218	12.6	217	2 JT0664	growth factor rece
15	202	11.7	228	2 S25730	SH2-SH3 protein se
16	184	10.6	1291	2 S00666	1-phosphatidylinos
17	182	10.5	1097	2 T31504	hypothetical prote
18	178	10.3	1290	2 A36466	1-phosphatidylinos
19	177	10.2	1290	2 A31317	transforming prote
20	172.5	10.0	839	1 TVHUV	hypothetical prote
21	170	9.8	816	2 T17257	transforming prote
22	167	9.6	844	2 TVMSV	transforming prote
23	165	9.5	1270	2 T09194	adaptor protein in
24	164	9.5	1196	2 T14108	SH3-containing pro
25	161	9.3	1094	2 T13053	dynamlin associated
26	158.5	8.9	330	2 JE0376	Grb-2 related adap
27	154.5	8.9	878	2 I51940	gene VAV2 protein
28	152.5	8.8	1011	2 T13055	dynamlin associated
29	151.5	8.7	334	2 T33836	hypothetical prote

30	151	8.7	1168	1 MMAXIC	myosin heavy chain
31	150	8.7	443	2 T27877	hypothetical prote
32	150	8.7	960	1 A39651	discs-large tumor
33	149.5	8.6	639	2 T13151	adaptor protein CM
34	148.5	8.6	1113	1 A47106	myosin heavy chain
35	148	8.5	290	2 T42526	hypothetical prote
36	147	8.5	1044	2 S01966	hypothetical prote
37	146.5	8.5	1038	2 JT0663	Grpase-activating
38	146	8.4	946	2 T38100	ras Grpase-activat
39	144.5	8.3	1047	2 A40121	Grpase-activat
40	143.5	8.3	870	2 B40121	Grpase-activating
41	142	8.2	450	2 A41973	protein-tyrosine k
42	141	8.1	665	2 JC7191	85k c-Cbl-interact
43	139.5	8.0	1236	1 A53970	1-phosphatidylinos
44	139	8.0	359	2 S27788	neutrophil oxidase
45	139	8.0	557	2 A00629	protein-tyrosine k

#### ALIGNMENTS

RESULT 1  
I58394  
c-Crk : mouse  
C:Species: Mus sp. (mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
C:Accession: I58394  
R:Ogawa, S.; Toyoshima, H.; Kozutsun, H.; Hagihara, K.; Sakai, R.; Tanaka, T.; Hiran  
Oncogene 9, 1669-1678, 1994  
A>Title: The C-terminal SH3 domain of the mouse c-Crk protein negatively regulates ty  
A:Reference number: I58394; M0ID:94239744  
A:Accession: I58394  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-304 <RES>  
A:Cross-references: GB:S7408; MTD:9632866; PIDN:AAB30755.1; PID:9632867  
C:Genetics:  
A:Gene: c-Crk  
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
F:139-118/Domain: SH2 homology <SH2>  
F:139-187/Domain: SH3 homology <SH3>

Query Match	Score	1612	DB 2	Length	304
Best Local Similarity	100.0%			Pred. No. 3.9e-113	
Matches	303		Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	5	AGNPDSEERSWYGRSLRQENAVALLQGGRGVFLYRDSSTSPGDVLSVSENSRSHYI 64			
DB	2	AGNPDSEERSWYGRSLRQENAVALLQGGRGVFLYRDSSTSPGDVLSVSENSRSHYI 61			
QY	65	INSSGPRPPVPPAPPPPCVSPSLRTGQDFPSLPALLEFKIHYLDPTTLIEPVARS 124			
DB	62	INSSGPRPPVPPAPPPPCVSPSLRTGQDFPSLPALLEFKIHYLDPTTLIEPVARS 121			
QY	125	RQSGSVILRQEAQYRALDFNGNDEEDLPFKGDIILRIKPEQWMAADSECKRM 184			
DB	122	RQSGSVILRQEAQYRALDFNGNDEEDLPFKGDIILRIKPEQWMAADSECKRM 181			
QY	185	IPPPYVEKYRPAASVSALIGNOBESHQPLGPPPGYAPQSVNTPLPINQNGPIYAR 244			
DB	182	IPPPYVEKYRPAASVSALIGNOBESHQPLGPPPGYAPQSVNTPLPINQNGPIYAR 241			
QY	245	VIOKRPNAVDTALALEVQELVKTKINVSQWEGECNGKRGHPFTVRLDDQNPDE 304			
DB	242	VIOKRPNAVDTALALEVQELVKTKINVSQWEGECNGKRGHPFTVRLDDQNPDE 301			
QY	305	DFS 307			
DB	302	DFS 304			
RESULT	2				

A45022  
 CRK-II - human  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 20-Jun-2000  
 C:Accession: A45022  
 R:Matsumura, M.; Tanaka, S.; Nagata, S.; Kojima, A.; Kurata, T.; Shibuya, M.  
 Mol. Cell. Biol. 12, 3482-3489, 1992  
 A:Title: Two species of human CRK cDNA encode proteins with distinct biological activities  
 A:Reference number: A45022; MUID:92334347  
 A:Accession: A45022  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-304 <MAT>  
 A:Cross-references: GB:D10656; NID:g219554; PIDN:BA01505.1; PID:g219555  
 A:Experimental source: placenta  
 A>Note: sequence extracted from NCBI backbone (NCBIN:108769, NCBIPI:108770)  
 C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
 F:13-119/Domain: SH2 homology #status atypical <SH2>  
 F:139-187/Domain: SH3 homology <SH3>

Query Match 91.6%; Score 1588; DB 2; Length 304;  
 Best Local Similarity 98.7%; Pred. No. 2.4e-111;  
 Matches 299; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYMGRLSROEAVALLQGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2 AGNFDSEERSWYMGRLSROEAVALLQGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 61  
 QY 65 INSSGPRPVPSPAPQPPGVSPSRRLRIGDQFDSLPALEFFKIHLYDTTLLIEPVARS 124  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 62 INSSGPRPVPSPAPQPPGVSPSRRLRIGDQFDSLPALEFFKIHLYDTTLLIEPVARS 121  
 QY 125 ROSSGVILROEAEVYRALFDENGNDDEDLPEFKGDLIRDKPEEQMNAEDSEGRGM 184  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 122 ROSSGVILROEAEVYRALFDENGNDDEDLPEFKGDLIRDKPEEQMNAEDSEGRGM 181  
 QY 185 IPVPYVEKYRPASASVSALIGNQEGSHPOPLGPEPGPYAQPVSNTPLPRLNONGPEYAR 244  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 182 IPVPYVEKYRPASASVSALIGNQEGSHPOPLGPEPGPYAQPVSNTPLPRLNONGPEYAR 241  
 QY 245 VIOKRPVNAVDTALALEVGLVYTKINVSQWEGECNGKRGHFFPTHVRLDQONPD 304  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 242 VIOKRPVNAVDTALALEVGLVYTKINVSQWEGECNGKRGHFFPTHVRLDQONPD 301  
 QY 305 DFS 307  
 ||||  
 Db 302 DFS 304

RESULT 3  
 A49011  
 c-Crk - chicken  
 C:Species: Gallus gallus (chicken)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A49011  
 R:Reichman, C.T.; Mayer, B.J.; Keshav, S.; Hanafusa, H.  
 Cell Growth Differ. 3, 451-460, 1992  
 A:Title: The product of the cellular crk gene consists primarily of SH2 and SH3 regions.  
 A:Reference number: A49011; MUID:93041379  
 A:Accession: A49011  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-305 <REI>  
 A:Cross-references: GB:L08168; GB:M32398; NID:g212527; PIDN:AAA49001.1; PID:g212528  
 A:Experimental source: embryo, brain  
 A>Note: sequence extracted from NCBI backbone (NCBIN:117106, NCBIPI:117107)  
 C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
 F:13-119/Domain: SH2 homology <SH2>  
 F:140-188/Domain: SH3 homology <SH3>

Query Match 79.6%; Score 1379.5; DB 1; Length 305;

Best Local Similarity 84.5%; Pred. No. 9e-96;  
 Matches 257; Conservative 19; Mismatches 27; Indels 1; Gaps 1;

QY 5 AGNFDSEERSWYMGRLSROEAVALLQGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2 AGNFDSEERSWYMGRLSROEAVALLQGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 61  
 QY 65 INSSGPRPVPSPAPQPPGVSPSRRLRIGDQFDSLPALEFFKIHLYDTTLLIEPVARS 123  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 62 INSSGPRPVPSPAPQPPGVSPSRRLRIGDQFDSLPALEFFKIHLYDTTLLIEPVARS 121  
 QY 124 ROSSGVILROEAEVYRALFDENGNDDEDLPEFKGDLIRDKPEEQMNAEDSEGRGM 183  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 122 ROSSGVILROEAEVYRALFDENGNDDEDLPEFKGDLIRDKPEEQMNAEDSEGRGM 181  
 QY 184 IPVPYVEKYRPASASVSALIGNQEGSHPOPLGPEPGPYAQPVSNTPLPRLNONGPEYAR 243  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 182 IPVPYVEKYRPASASVSALIGNQEGSHPOPLGPEPGPYAQPVSNTPLPRLNONGPEYAR 241  
 QY 244 VIOKRPVNAVDTALALEVGLVYTKINVSQWEGECNGKRGHFFPTHVRLDQONPD 303  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 242 VIOKRPVNAVDTALALEVGLVYTKINVSQWEGECNGKRGHFFPTHVRLDQONPD 301  
 QY 304 EDFS 307  
 ||||  
 Db 302 EDFS 305

RESULT 4  
 A46243  
 epidermal growth factor-receptor-binding protein GRB-3 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 12-Feb-1999  
 C:Accession: A46243  
 R:Margolis, B.; Silvenoinen, O.; Comoglio, F.; Roonprapant, C.; Skolnik, E.; Ullrich  
 Proc. Natl. Acad. Sci. U.S.A. 89, 8894-8898, 1992  
 A:Title: High-efficiency expression/cloning of epidermal growth factor-receptor-binding  
 A:Reference number: A46243; MUID:93028373  
 A:Accession: A46243  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-239 <MAR>  
 A>Note: sequence extracted from NCBI backbone (NCBIPI:115326)  
 C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
 C:Keywords: growth factor receptor  
 F:44-149/Domain: SH2 homology <SH2>  
 F:170-218/Domain: SH3 homology <SH3>

Query Match 62.2%; Score 1078; DB 2; Length 239;  
 Best Local Similarity 99.5%; Pred. No. 2.1e-73;  
 Matches 206; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AGNFDSEERSWYMGRLSROEAVALLQGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 64  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 33 AGNFDSEERSWYMGRLSROEAVALLQGRHGVFLVRDSTSPGDYVLSVSENRSVSHYI 92  
 QY 65 INSSGPRPVPSPAPQPPGVSPSRRLRIGDQFDSLPALEFFKIHLYDTTLLIEPVARS 124  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 93 INSSGPRPVPSPAPQPPGVSPSRRLRIGDQFDSLPALEFFKIHLYDTTLLIEPVARS 152  
 QY 125 ROSSGVILROEAEVYRALFDENGNDDEDLPEFKGDLIRDKPEEQMNAEDSEGRGM 184  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 153 ROSSGVILROEAEVYRALFDENGNDDEDLPEFKGDLIRDKPEEQMNAEDSEGRGM 212  
 QY 185 IPVPYVEKYRPASASVSALIGNQEGS 211  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 213 IPVPYVEKYRPASASVSALIGNQEGS 239

RESULT 5  
 B45022  
 CRK-I - human



A:Reference number: A44988; MUID:90045469  
A:Accession: A44988  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-259 <TSU>  
A:Cross-references: GB:X17292  
A:Note: the authors translated the codon CGG for residue 79 as Gly, and CAG for residue 81  
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
F:67-173/Domain: SH2 homology <SH2>  
F:194-242/Domain: SH3 homology <SH3>

Query Match	48.28;	Score 834.5;	DB 2;	Length 259;
Best Local Similarity	78.38;	Pred. No. 3.5e-55;		
Matches 159;	Conservative 17;	Mismatches 26;	Indels 1;	Gaps 1

[illegible]

RESULT 9  
TFVFL10  
transforming protein crk - avian sarcoma virus C710  
C:Species: avian sarcoma virus C710  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 03-Mar-1995  
C:Accession: B29851  
R:Mayer, B.J.; Hamauchi, M.; Hanafusa, H.  
Nucleu 332, 272-275, 1988  
A>Title: A novel viral oncogene with structural similarity to phospholipase C  
A:Reference number: S00872; M0ID:88156964  
A:Accession: B29851  
A:Molecule type: genomic RNA  
A:Residues: 1-232 <MAY>  
A:Cross-references: EMBL:Y00302  
C:Genetics:  
A:Gene: crk  
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
C:Keywords: transforming protein  
E:40-146/Domain: SH2 homology #status atypical <SH2>  
E:167-215/Domain: SH3 homology <SH3>

Query Match	47.28;	Score 818.5;	DB 1;	Length 232;
Best Local Similarity	77.38;	Pred. No. 4.8e-54;		
Matches 157;	Conservative 16;	Mismatches 29;	Indels 1;	Gaps 1

[illegible]

Db 209 MIPVPVEKCRSSASVSTLTGG 231

```

RESULT 10
A46444
SH2-SH3 adaptor protein drk - fruit fly (Drosophila melanogaster)
N:Alternate names: gene drk protein
C:Species: Drosophila melanogaster
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 03-Dec-1999
C:Accession: A46444; A46443
R:Olivier, J.P.; Raabe, T.; Henkemeyer, M.; Dickson, B.; Mhamdi, G.; Marqolli, B.; S
Cell 73, 179-191, 1993
A>Title: A Drosophila SH2-SH3 adaptor protein implicated in coupling the sevenless ty
A:Reference number: A46444; MUID:93214990
A:Accession: A46444
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <OLI>
A>Note: sequence extracted from NCBI backbone (NCBIN:128546, NCBI:P:128547)
R:Simon, M.A.; Dodson, G.S.; Rubin, G.M.
Cell 73, 169-177, 1993
A>Title: An SH3-SH2-SH3 protein involved for p21Ras1 activation and binds to seven
A:Reference number: A46443; MUID:93214989
A:Accession: A46443
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-211 <SIM>
A:Cross-references: GB:L12446; NID:g304808; PID:g304809
A>Note: sequence extracted from NCBI backbone (NCBI:P:128545)
C:Genetics:
A:Gene: drk; E(sev)2B
A:Cross-references: FlyBase:FBgn0004638
A:Note: Downstream of Receptor Kinases (drk)
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology
E:60-149/Domain: SH2 homology <SH2>
E:159-206/Domain: SH3 homology <SH3>

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Query Match	13.68;	Score 236;	DB 2;	Length 211;
Best Local Similarity	29.68;	Pred. No. 1.3e-10;		
Matches	56;	Conservative	37;	Mismatches 64;
				Indels 32;
				Gaps 5

```

OY      7 NFDEEESWMYRKLISROCAVALLQOGHGFVALRODSTSPGGYLVASVENSRSHTIIN 66
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      51 NYIMKMHDMYGRITRADAEKLLSNKEGAFILRISESPPGSFSLVCPCDGOHEFVL 110
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      67 SSGRRPVPSRPQPPGYSERLIRGQEDDSLPALLEYKIHNYIDTTLLEPARSRQ 126
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      111 RD-----AQSFLVMYKNSINELVEYHR-----TATSRSD 144
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY      127 GSGVILRQ--EEAEVRALDEFNGNDEEDLPFKKGDIILIRDRPEOMNAEDSGCKRM 184
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      145 ---VKRLDMIPEMLQAYLDVPDESSEIDFRGQGIIVTDSDSNNWGNCIG--NRGI 200
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

QY	185	IPVPYVEKY	193
		↓ ↓ ↓	
Db	201	FPATYVTPY	209

RESULT 11  
S26050  
growth factor receptor-bound protein, GRB2 - rat  
N.Alternate names: Ash-m; Ash-s; gene ash protein  
C.Species: Rattus norvegicus (Norway rat)  
C.Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text\_change 21-Jan-2000  
C.Accession: S26050; I55429; I70120  
R.Matuko, K.; Shidata, M.; Yamakawa, A.; Takenawa, T.  
Proc. Natl. Acad. Sci. U.S.A. 89, 9015-9019, 1992  
A.Title: Cloning of SCH, a ubiquitously protein composed of one Src homology region (SH  
A.Reference number: S26050; MUID:93028395  
A.Accession: S26050  
A.Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-217 <MAT>  
A:Cross-references: EMBL:X62853; NID:g955762; PIDN:CAA44665.1; PID:g955763  
J.Matlanabe, K.; Fukuchi, T.; Hosoya, H.; Shirasawa, T.; Matuoka, K.; Miki, H.; Takenawa,  
T. Biol. Chem. 270, 13733-13739, 1995  
A:Title: Splicing isoforms of rat AshGrpD. Isolation and characterization of the cDNA  
A:Reference number: 155429; MUID:95293967  
A:Accession: 155429  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-156, 171-217 <RES>  
A:Cross-references: GB:D49846; NID:g914956; PIDN:BAA08645.1; PID:g914957  
A:Accession: I70120  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-59 <RE2>  
A:Cross-references: GB:D49847; NID:g914960; PIDN:BAA08646.1; PID:g914961  
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
C:Keywords: growth factor receptor  
F:5-53/Domain: SH3 homology <SH31>  
F:60-150/Domain: SH2 homology <SH2>  
F:163-210/Domain: SH3 homology <SH32>

Query Match	12.9%;	Score 224;	DB 2;	length 217;
Best Local Similarity	27.9%;	Pred. No. 1e-09;		
Matches	53;	Conservative	44;	Mismatches 57;
				Indels 36;
				Gaps 7;

```

OY 7 NFDSEBSRWGSLRQEAALLQGRH-CVFLVROSSSTSPGDYLVASVENSRYHII 65
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 51 NYIEMKPRHPEFGKIPRAKAEEMLSKORHDAFLIRSESAPGDFSLSVKFGNDYOHFKV 110
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 66 NSSGCRPVPPSPAPPPGVSPSRLIRGDOFDSLPLLEFYKIHLYDITTLLEPARSR 125
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 111 LRDS-----AGKFLMYVYKFNLSLNLVDYHR-----SIS-----VSRNQ 144
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 126 QGSGVILRQ-----EEAEYRALPDFNGNDEEDLPFKKQILRLRDKPBEOMNAEDSEG 180
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 145 Q---LFLRDIEQVPOQPLFYVALPDFPOQEDGELGFRRGDFIHMONSDNMMWKA-CHG 200
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 181 KRGMIPIVYV 190
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 201 QTGMFPRMYV 210
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 12  
A54688  
modular adaptor Grb2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 21-Jan-2000  
C:Accession: A54688  
R:Sun, K.L.; Bustelo, X.R.; Pawson, T.; Barbacid, M.  
Mol. Cell. Biol. 13, 5500-5512, 1993  
A:Title: Molecular cloning of the mouse grb2 gene: differential interaction of the Grb2  
A:Reference number: A54688; MUID:93360585  
A:Accession: A54688  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-217 <SUE>  
A:Cross-references: GB:U07617; NID:g464004; PIDN:AAB40022.1; PID:g464005  
C:Genetics:  
A:Gene: grb2  
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
F:5-33/Domain: SH3 homology <SH31>  
F:60-150/Domain: SH2 homology <SH2>  
F:163-210/Domain: SH3 homology <SH32>

Query Match	12.9%	Score 224	DB 2	Length 217
Best Local Similarity	27.9%	Pred. No. 1e-09		
Matches 53; Conservative	44;	Mismatches 57;	Indels 36;	Gaps 7.

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Db      51 NIEMKPPHWEFGKIPRAKAEMLSKORHDAFLIRESESAPGDFSLVFGNDVQHFKV 110
QY      66 NSSGRPPVPSPAPPPGVSFSLRIGDQGFDSLPLALLEFKYKHYYDTTLLEPARSR 125
Db      111 LRDG-----AGRYFLVMVYFNSLNLVLYYHR-----STS-----VSRNO 144
QY      126 QGSGVILRQ-----EAAFYRALPDFNGNDEEDLPFKKGLRLIRQKPEEGMNAEESG 180
Db      145 Q--TEFLNDIEQMQLPYVALPDFDEQEDGELGFRGDFIHVMNDSNDPMWKA-CHG 200
QY      181 KRGMIPIVYV 190
Db      201 QTGMFPRNVV 210

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RESULT 13  
A43321  
growth factor receptor-bound protein 2 - human  
N:Alternate names: abundant-src-homology (ash) protein  
N:Contains: growth factor receptor-bound protein 3.3  
C:Species: Homo sapiens (man)  
C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: A43321; A54064; A46278  
R:Rosenstein, E.J.; Daly, R.J.; Batzer, A.G.; Li, W.; Margolis, B.; Lammers, R.; Ullr  
Cell 70, 433-442, 1992  
A:Article: The SH2 and SH3 domain-containing protein GRB2 links receptor tyrosine kinas  
A:Reference number: A43321; MUID:92354060

A:Cross-references: GB:W66995; NID:g181975; PIDN:AAA58448.1; PID:g181976  
A:Experimental source: brain  
A>Note: sequence extracted from NCBI backbone (NCBIN:110294, NCBITP:110295)  
R:Faeh, I.; Schweighofer, F.; Rey, I.; Multon, M.C.; Boltzane, J.; Duchesne, M.; Toog  
Science 264, 971-974, 1994  
A>Title: Cloning of a Grb2 isoform with apoptotic properties.  
A:Reference number: A54064; MUID:94233382  
A:Accession: A54064  
A:Molecule type: mRNA  
A:Residues: 1-59,101-217 <FAT>  
A:Cross-references: GB:I29511; NID:g460667; PIDN:AAC37549.1; PID:g498178  
R:Matukwa, K.; Shihara, M.; Yamakawa, A.; Takemura, T.  
Proc. Natl. Acad. Sci. U.S.A. 89, 9015-9019, 1992  
A>Title: Cloning of ASH, a ubiquitous protein composed of one Src homology region (SH  
A:Reference number: S26050; MUID:93028395  
A:Accession: A46278  
A:Molecule type: mRNA  
A:Residues: 58-217 <MAT>  
A:Cross-references: EMBL:X62852; NID:g28875; PIDN:CAA44664.1; PID:g28876  
C:Genetics:  
A:Gene: GDB:GRB2  
A:Cross-references: GDB:I34732; OMIM:600180  
A:Map position: 17q24-17q25  
C:Superfamily: crk transforming protein; SH2 homology; SH3 homology  
C:Keywords: alternative splicing; growth factor receptor  
F:1-217/Product: growth factor receptor-bound protein 2 #status predicted <LSF>  
F:1-59,101-217/Product: growth factor receptor-bound protein 3-3 #status predicted <S  
F:5-53/Domains: SH3 homology <SH3L>  
F:60-150/Domains: SH2 homology <SH2>  
F:163-210/Domains: SH3 homology <SH32>

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Query Match      12.9%  Score 224;  DB 2;  Length 217;
Best Local Similarity 27.9%;  Pred. No. 1e-09;
Matches 53;  Conservative 44;  Mismatches 57;  Indels 36;  Gaps 7;

QY 7 NFDEERSNMYWRGLRQREAVALLGQRH-GVELRDSTSPGDYLVSENSRSHYII 65
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Db 51 NYIMKRRHPFFGKIRAKAEKLSQRIDGAFLLREESKPGPFSLVFGMDVQHFV 110
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
QY 66 NSSGPRPVPSPDAPPPGVSSRLRIGDQEDDSIPLALEEYKTHYLDTTLLIEPVARS 125
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :

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